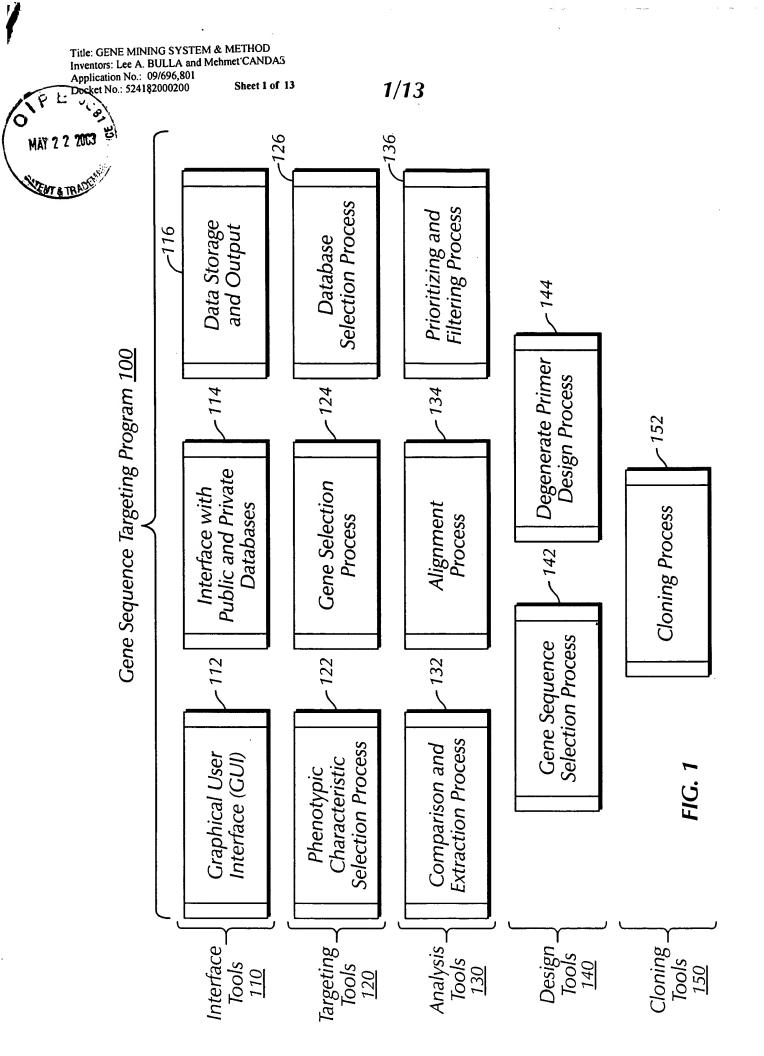
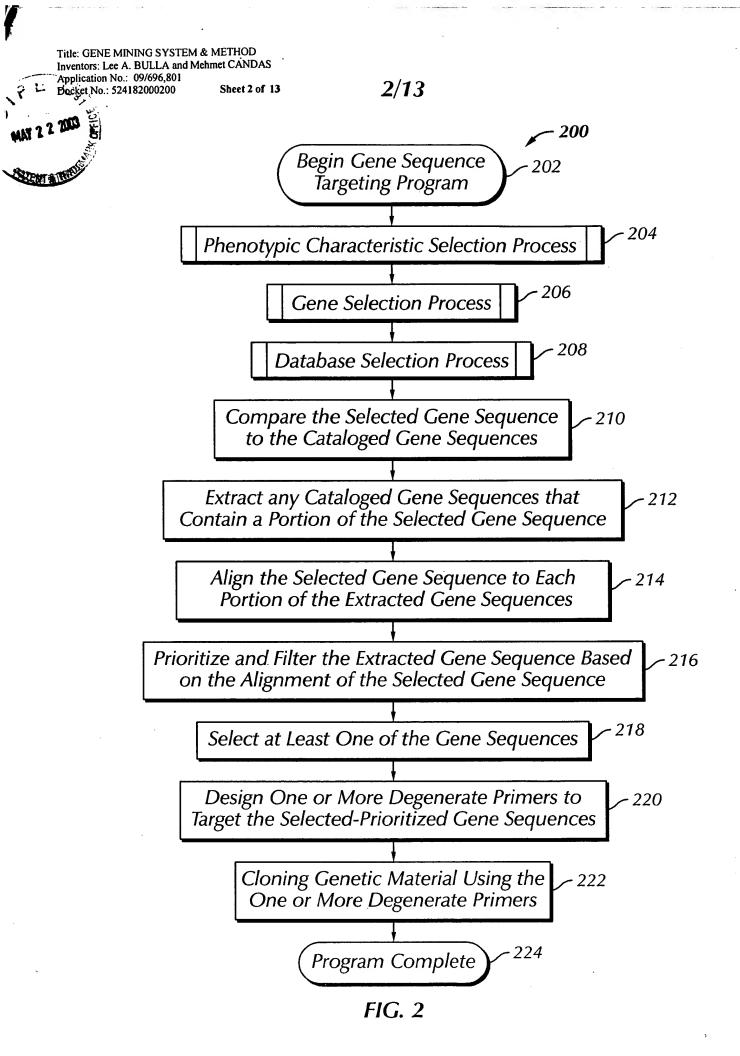
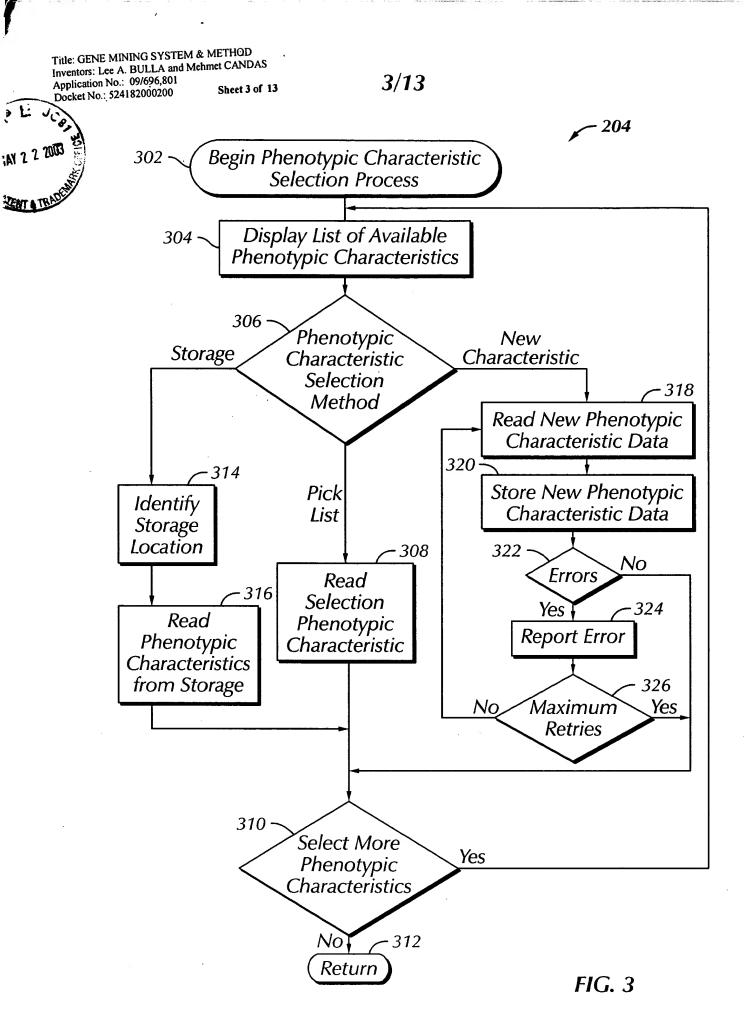
DRAWINGS AMENDMENTS

The attached 13 sheets of drawings include changes to the numbering of Figures 7-14. Figure 8 is now 7; Figure 9 is now 8; Figure 10 is now 9; Figure 11 is now 10; Figure 12 is now 11; Figure 13 is now 12; and Figure 14 is now 13.







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Return

FIG. 4

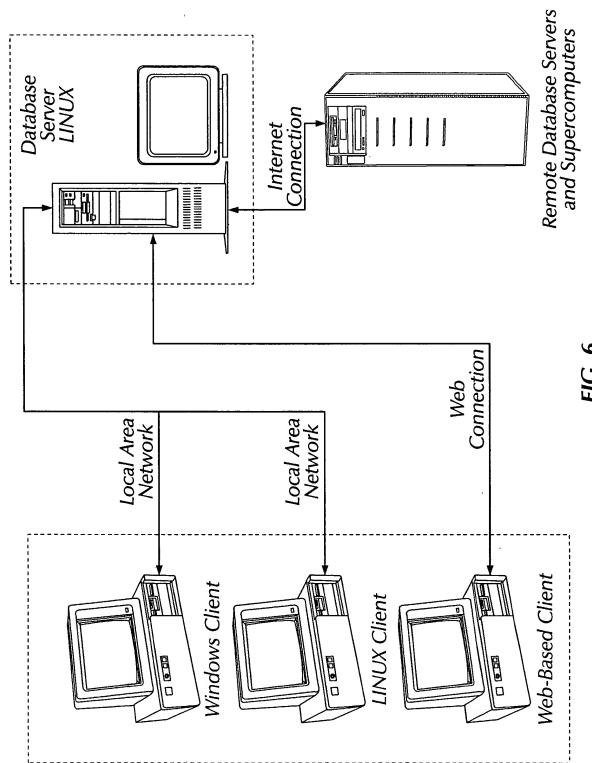
Title: GENE MINING SYSTEM & METHOD Inventors: Lee A. BULLA and Mehmet CANDAS Application No.: 09/696,801 5/13 Sheet 5 of 13 Docket No.: 524182000200 *208* Begin Database 502 Selection Process 504 -Display List of Available Databases **Pick** New Database List **Database** Selection -518 Method 506 Read New Database Data 520 508 Store New Read Selection Database Data Database from GUI 522 -510 No **Errors** Display List of Available Superfamilies, Families Yes 524 and Subfamilies in Report Error Selected Database -512 526 Read Selected Superfamilies, Families No Maximum or Subfamilies from GUI Retries Yes 514 -Select Yes Another **Database** No 516 FIG. 5 Return

4

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Sheet 6 of 1

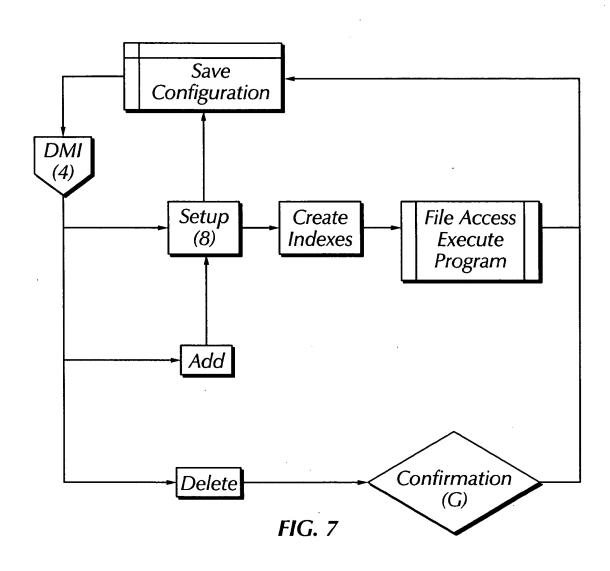
2 2053

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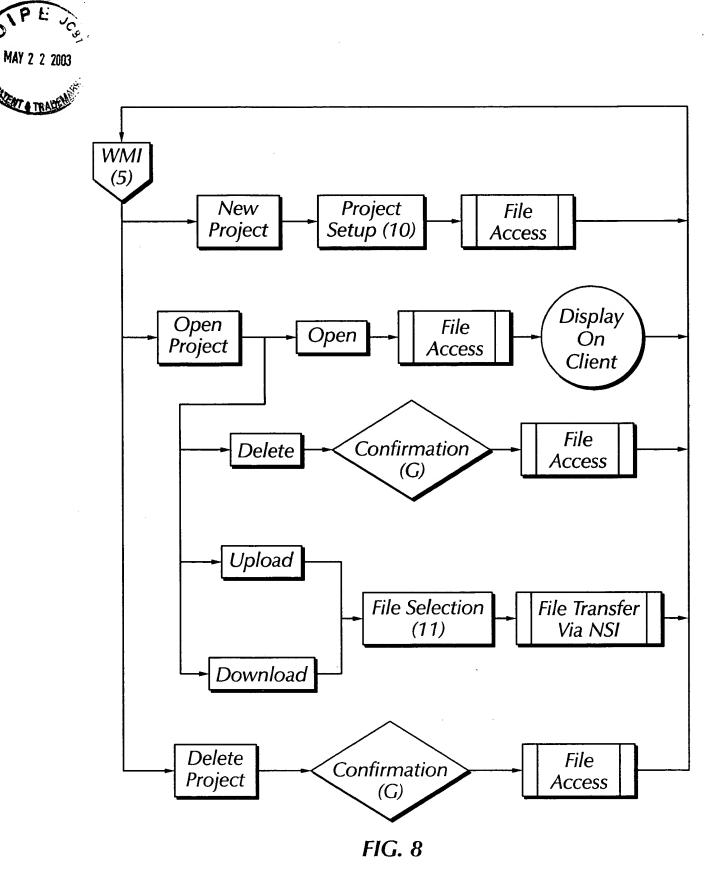
Sheet 7 of 13





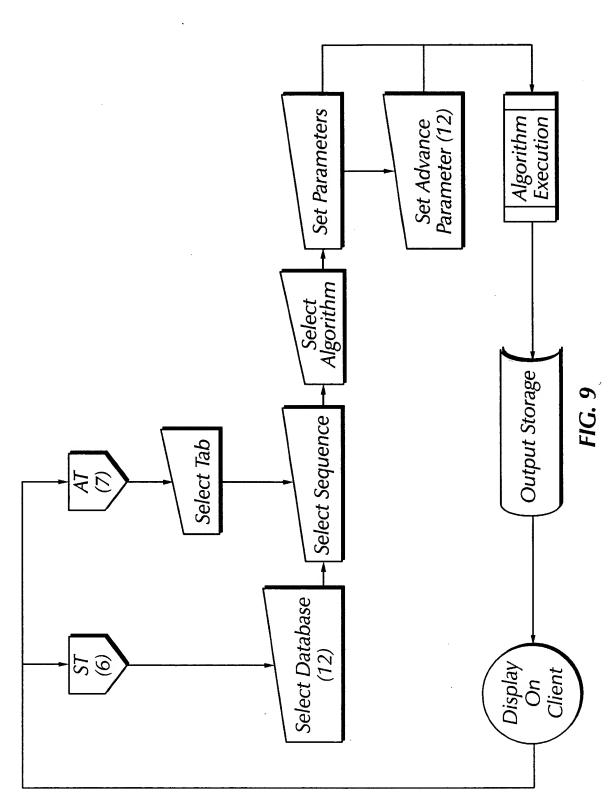
Application No.: 09/696,801 Docket No.: 524182000200

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Docket No.: 524182000200

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Sheet 10 of 13

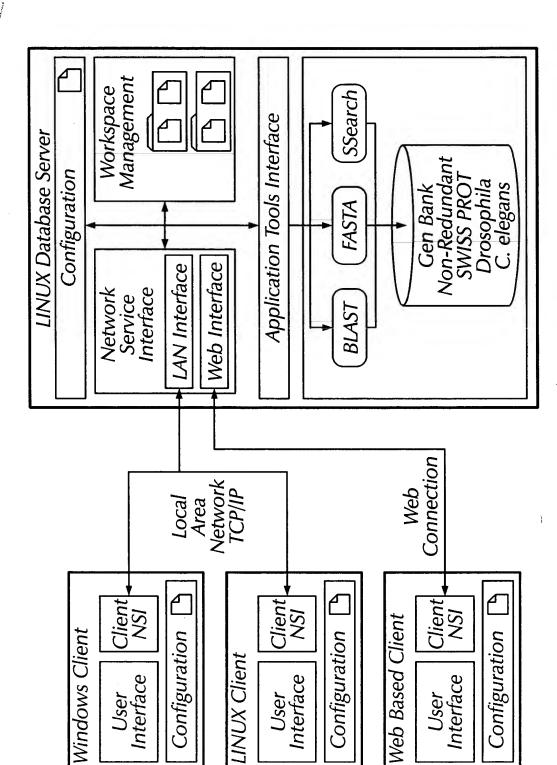
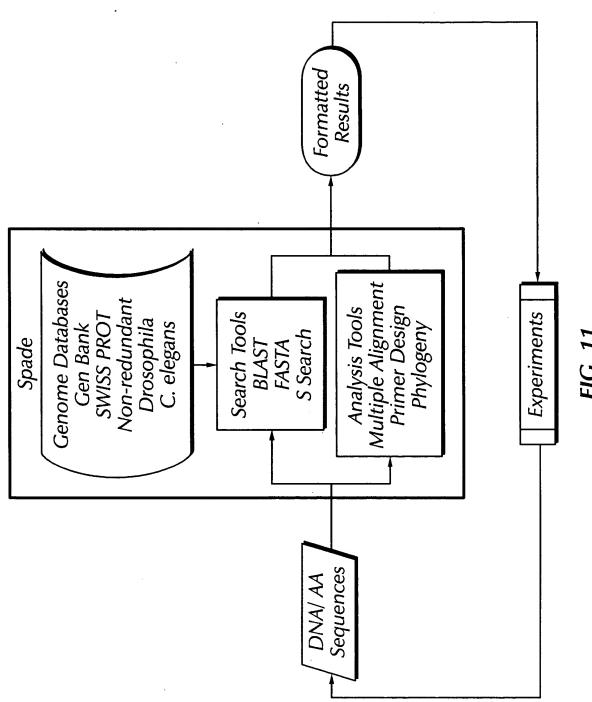


FIG. 10

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HG. 11

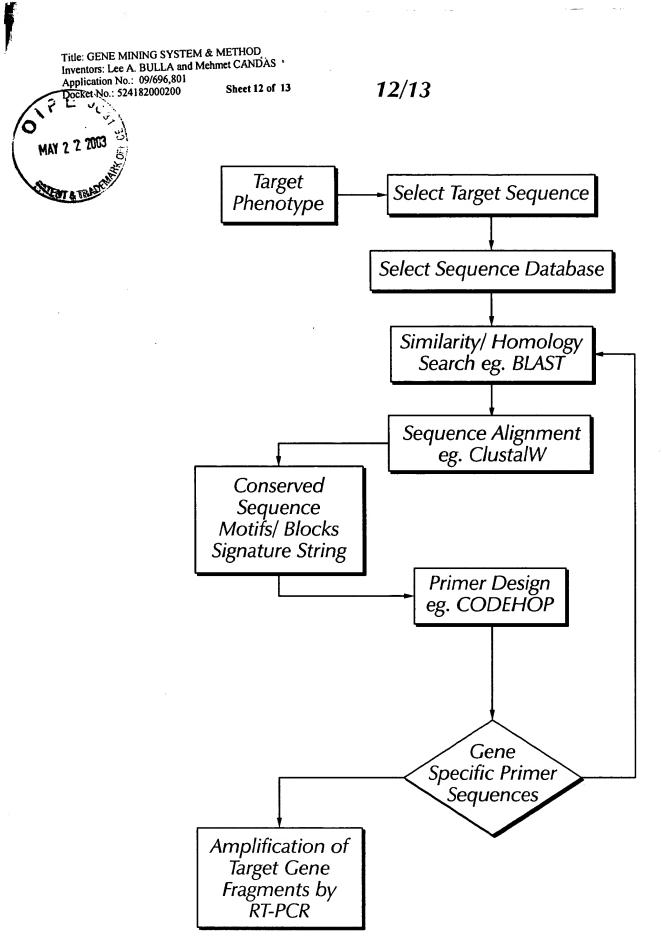


FIG. 12

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70 KGGFDAIMQVMTCEKEIGWRPGSR GCGTATAATTGTTCTGTGCACCGATTCCCCATATCACAGCGCTGGTGACGGCAAAATGATAGGCATTATC140 RIIVLCTDSPYHSAGDGKMIGII AAACCCAACGACATGTTATGCCACTTAAAGGGACAAAAATATGAAGCAGAAATGGCCCCAAGATTATCCAT 210 K P N D M L C H L K G Q K Y E A E M A Q D Y P CTGTGAGTAAAATAAATAAAGTAGCAAAGCAAGGAAAATTCGGTATCATATTCGCTGCTTTTGGCTGAGGT 280 S V S K I N K V A K Q G K F G I I F A A L A E V CCGTGATGTTTATACCTTGTTAGCGGAACAAATAGTCGGAGCTGAGTACGCCGAACTGAAGAAACAGAAG 350 R D V Y T L L A E Q I V G A E Y A E L K K Q K TCAAATATTGTAGAGATCATTATAAAAGCGTACCAACGCAGCGTTCGAAGTATCAAATTGGATTATGACA 420 S N I V E I I I K A Y Q R S V R S I K L D Y D 490 I P S F V R L K L N Q S C D G T P I N C A S T Y TGAAAATCCAGTGGTTACAATTCCGGCTATTCTAGAGGTTAAAGAATGTCCTAAAGAAAATAAAACACAT 560 ENPVVTIPAILEVKECPKENKTH GAGCTTGTTATTAACCCTGTGTCTTTAAATGACAAATTAATAATTAAATTGGAAGTCATCTGTAAATGTG 630 ELVINPVSLNDKLIIKLEVICKC **ACTGTGAAGTCAAAAGTGATATAAGTTCAAGATGTAATAATGCAGGATATATACAGTGTGGTATCTGCAA** 700 D C E V K S D I S S R C N N A G Y I Q C G I C K GTGTCTCGATTCAAGTTATGGCGACGAATGTCAGTGCAGCGTTACATCTTCGGGGGGTGGCTAATAAGGAG 770 C L D S S Y G D E C Q C S V T S S G V A N K E 840 K D D A K C R K D L N D I V L C S G K G V C M GTGGTAAATGTACTTGTAACCCTGATCGTTCAGGAAAATATTGCGAATTTGACGATAAGGCATGCGATAA 910 C G K C T C N P D R S G K Y C E F D D K A C D N ${\tt TCTTTGCTCAAACCATGGGATTTGTACCTTAGGCTCATGCCAGTGCGATAGCGGTTGGTCTGGAAATGAT}$ 980 L C S N H G I C T L G S C Q C D S G W S G N D TGCGGTTGTCCAACTAGTAACACAGACTGCTACGCTCAATACTCTGAGGAGGTTTGTTCTGGCAACGGTG 1050 C G C P T S N T D C Y A Q Y S E E V C S G N G AATGTGTATGCGGAAATGCCAATGTGCGAAGGTTAAAGGAAAAAACGAAACGTACGCAGGAGTATTTTGT 1120 ECVCGNANVRRLKEKTKRTQEYFV GACACATGCAATGACTGCCAATCAAAATATTCTAAAGCCCTCGAACCAAATGTAGAATGTAACTACATAC 1190 T H A M T A N Q N I V K P S N Q M . N V T T Y AAGGTCTAGAAACTTGTGATAAGATTTACAACAATACAGAAAACAATGTTGTTATAAAAATGGTCAACAA 1260 K V . K L V I R F T T I Q K T M L L . K W S T AACAGAAATTAATTCGCCTAAATGGAGTGGCGCTACTTGGTGCAAAAAAGTAATAGAGGACGGCAGTTTT 1330 K Q K L I R L N G V A L L G A K K . . R T A V L ATAATATTCAGATATTATCATAACGCAACGACGCACGGGTTGCATATAATCATTCAAACGGAACCAGAGG 1400 Y S D I I I T Q R R T G C I . S F K R N Q R CACCTCCAATAGGAAATAAGTGGATTGCCCTCATCAGTTGCATAGTGGCTGTAGTACTCATTGGCTTGTT 1470 H L D . E I S G L P S S V A . W L . Y S L A C GACGTTGATTGCGTGGAAGATCCTCGTAGACTTGCACGATAAAAGGGAATATGCCAAGTTGA 1532 . R . L R G R S S . T C T I K G N M P S .